

CLUSTAL W (1.83) Multiple Sequence Alignments

Sequence format is Pearson

Sequence 1: SEQ174 334 aa

Sequence 2: G_kaustophilus 378 aa

Start of Pairwise alignments

Aligning...

Sequences (1:2) Aligned. Score: 97

Guide tree file created: [/ebi/extserv/clustalw-work/interactive/clustalw-20060731-05543637.dnd]

Start of Multiple Alignment

There are 1 groups

Aligning...

Group 1: Sequences: 2 Score:6996

Alignment Score 1906

CLUSTAL-Alignment file created [/ebi/extserv/clustalw-work/interactive/clustalw-20060731-05543637.aln]

```

SEQ174 -----NSDISIIIESFIPL 13
G_kaustophilus MNISIDREALAKSVQDVMKAVSTRRTTIPILTGIKLTATASGVTLTGSDSDIS-IESFIPL 59
                      :****

SEQ174 EKEGKLLVDVKRPGSIVLQARFFSEIVKKLPQQTVEIETEDNFLTIIIRSGHSEFRLNGLN 73
G_kaustophilus EKEGKLLVDVKRPGSIVLQARFFSEIVKKLPQQTVEIETEDNFLTIIIRSGHSEFRLNGLN 119
                      *****

SEQ174 ADEYPRLPQIEEENVFQIPADLLKTIVIRQTVFAVSTSETRPILTGVNWKVEHGELVCTAT 133
G_kaustophilus ADEYPRLPQIEEENVFQIPADLLKTIVIRQTVFAVSTSETRPILTGVNWKVEHGELVCTAT 179
                      *****

SEQ174 DSHRLAMRKVKIIESENEVSYNVVIPGKSLNELSKIILDDGNHPVDIVMTANQVLFKAEH 193
G_kaustophilus DSHRLAMRKVK-IESENEVSYNVVIPGKSLNELSK-ILDDGNHPVDIVMTANQVLFKAEH 237
                      *****

SEQ174 LLFFSRLLDGNYPETARLIPTESKTTMIVNAKEFLQAI DRASLLAREGRNNVVKLTTLPG 253
G_kaustophilus LLFFSRLLDGNYPETARLIPTESKTTMIVNTKEFLQAI DRASLLAREGRNNVVKLTTLPG 297
                      *****

SEQ174 GMLEISSISPEIGKVTEQLQTESLEGEELNISFS AKYMMDALRALDGTDIQISFTGAMRP 313
G_kaustophilus GMLEISSISPEIGKVTEQLQTESLEGEELNISFS AKYMMDALRALDGTDIQISFTGAMRP 357
                      *****

SEQ174 FLLRPLHTDSMLQLILPVRTY 334
G_kaustophilus FLLRPLHTDSMLQLILPVRTY 378
                      *****

```

CLUSTAL W (1.83) Multiple Sequence Alignments

Sequence format is Pearson

Sequence 1: SEQ174 334 aa

Sequence 2: B_cereus 379 aa

Start of Pairwise alignments

Aligning...

Sequences (1:2) Aligned. Score: 70

Guide tree file created: [/ebi/extserv/clustalw-work/interactive/clustalw-20060731-05564381.dnd]

Start of Multiple Alignment

There are 1 groups

Aligning...

Group 1: Sequences: 2 Score:6158

Alignment Score 1389

CLUSTAL-Alignment file created [/ebi/extserv/clustalw-work/interactive/clustalw-20060731-05564381.aln]

```

SEQ174      -----NSDISI-IESFIPLE 14
B_cereus    MRFTIQKDYLVRSVQDVMKAVSSRTTIPILTGIVVATEEGVTLTGSADADISIESFIPVE 60
              .** . * *****;*

SEQ174      KEGKLLVDVKRPGSIVLQARFFSEIVKKLPQQTVEIETEDNFLTIIIRSGHSEFRLNGLNA 74
B_cereus    EDGKEIVEVKQSGSIVLQAKYFSEIVKKLPKETVEISVENHLMTKITSGKSEFNLNGLDS 120
              :*** :*:***:*****:*****:*****:*****:*****:*****:*****:

SEQ174      DEYPRLPQIEEENVFQIPADLLKTVIRQTVFAVSTSETRPILTGWNWKVEHGEVLVCTATD 134
B_cereus    AEYPLLPQIEEHHVFKEIPTDLLKHMIRQTVFAVSTSETRPILTGWNWKVYNSELTCIATD 180
              *** *****:***:***:*** :*****:*****:*****:*****:*****:

SEQ174      SHRLAMRKVKIIESENEVSYNVVIPGKSLNELSKIILDDGNHPVDIVMTANQVLFKAHL 194
B_cereus    SHRLALRKAKIEGIADEFQANVVIPGKSLNELSK-ILDESEEMVDIVITEYQVLFRTKHL 239
              *****:***:*** :*.. ***** *****:***:***:*****:***:

SEQ174      LFFSRLLDGNYFPETARLIPTESKTTMIVNAKEFLQAIDRASLLAREGRNNVVKLTTLPGG 254
B_cereus    LFFSRLLEGNYPDTRRLIPAESKTDIFVNTKEFLQAIDRASLLARDGRNNVVKLSTLEQA 299
              *****:***:***:***:*** :***:*****:*****:*****:*****:

SEQ174      MLEISSISPEIGKVTEQLQTESLEGEELNISFSAKYMMDALRALDGTDIQISFTGAMRPF 314
B_cereus    MLEISSNSPEIGKVVEEVQCEKVDGEELKISFSAKYMDALKALDSTEIKISFTGAMRPF 359
              ***** *****:***:***:***:*****:*****:*****:*****:*****:

SEQ174      LLRPLHTDSMLQLILPVRTY 334
B_cereus    LIRTVNDESIIQLILPVRTY 379
              ***:*** :*:*****
    
```

CLUSTAL W (1.83) Multiple Sequence Alignments

Sequence format is Pearson
 Sequence 1: SEQ174 334 aa
 Sequence 2: B_thuringiensis 379 aa
 Start of Pairwise alignments
 Aligning...
 Sequences (1:2) Aligned. Score: 70
 Guide tree file created: [/ebi/extserv/clustalw-work/interactive/clustalw-20060731-06031038.dnd]
 Start of Multiple Alignment
 There are 1 groups
 Aligning...
 Group 1: Sequences: 2 Score:6155
 Alignment Score 1387
 CLUSTAL-Alignment file created [/ebi/extserv/clustalw-work/interactive/clustalw-20060731-06031038.aln]

```

SEQ174      -----NSDISI-IESFIPLE 14
B_thuringiensis MRFSIQKDYLVRSVQDVMKAVSSRTTIPILTGIVVATEEGVTLTGSDADISIESFIPVE 60
               .** .* *****;

SEQ174      KEGKLLVDVKRPGSIVLQARFFSEIVKKLPQQTVEIETEDNFLTIIRSGHSEFRLNGLNA 74
B_thuringiensis EDGKEIVEVKQSGSIVLQAKYFSEIVKKLPKETVEISVENHMLTKITSGKSEFNLNGLDS 120
               :.* :*:.*:*****:*****:*****:*****:*****:*****:
               :.* :*:.*:*****:*****:*****:*****:*****:*****:

SEQ174      DEYPRLPQIEEENVFQIPADLLKTIVIRQTVFAVSTSETRPILTGIVNWKVEHGELVCTATD 134
B_thuringiensis AEYPLLPQIEEHHVFKIPTDLLKHMIRQTVFAVSTSETRPILTGIVNWKVYNSELTCIATD 180
               *** *****:.*:.*:***** :*****:*****:*****:*****:
               :.*:.* *****

SEQ174      SHRLAMRKVKIIESENEVSYNVVIPGKSLNELSKIILDDGNHPVDIVMTANQVLFKAHL 194
B_thuringiensis SHRLALRKAKIEGIVDEFQANVIPGKSLNELSK-ILDESEEMVDIVITEYQVLFRTKHL 239
               *****:.*.*** :*. ***** ***** :*. *****:
               :.* *****

SEQ174      LFFSRLLDGNYPETARLIPTESKTTMIVNAKEFLQAI DRASLLAREGRNNVVKLTTPGG 254
B_thuringiensis LFFSRLLLEGNYPDTRLI PAESKTDIFVNTKEFLQAI DRASLLARDGRNNVVKLTSTLEQA 299
               *****:*****:.*:*****:***** :*:*****:*****:*****:
               *****:*****

SEQ174      MLEISSISPEIGKVTEQLQTESLEGEELNISFSKYMMDALRALDGTDIQISFTGAMRPF 314
B_thuringiensis MLEISSNSPEIGKVVEEVQCEKVDGEELKISFSKYMMDALKALDSTEIKISFTGAMRPF 359
               ***** *****:.*:.* :*:*****:*****:*****:*****:
               *****

SEQ174      LLRPLHTDSMLQLILPVRTY 334
B_thuringiensis LIRTVNDESIQLILPVRTY 379
               *:.*: :*:*****
  
```

Sequence format is Pearson

Sequence 2: *B. weihenstephanensis* 381 aa

Aligning...

```
Guide tree      file created:  [/ebi/extserv/clusterlw-work/interactive/clusterlw-
20060731-06054661.dnd]
```

There are 1 groups

Aligning...

Alignment Score 1374

CLUSTAL-Alignment file created [/ebi/extserv/clustalw-work/interactive/clustalw-20060731-06054661.aln]

```

SEQ174
B_weihenstephanensis
-----NSDISI-IESFIPLE 14
MRFTIQKDYLVRSVQDVMKAVSSRTTIPILTGIKVVATEEGVTLTGSDADISIESFIPVE 60
          ** . * *****:*
```

SEQ174 KEGKLLVDVKRPGSGIVLQARFFSEIVKKLPQQTVEIETEDNFLTIIRSGHSEFRLNGLNA 74
B._weihenstephanensis DAGKEIVEIEQGSGSIILQAKYFSEIVKKLPKETVEISVENHFMTKIKSCKSEFNGLDA 120
 . ** :*:~::~**:*~::*****~::~***.~::~*~::~****~::~*

SEQ174
_weihenstephanensis

DEYFRLPQIEENVFQIPADLLKTIVIRQTVFAVSTSETRPILTVGNWVKVEHSELVCTATD 134
AEYPLLPQIEHHVFKIPTDLLKHMIRQTVFAVSSSETRPILTVGNWVKVYNSELTCIATD 180
*** ***,*:*:*:*** :*****:*****:*** **

EQ174 SHRLAMRKVKIIIES--ENEVSYNVVIPGKSLNELSKIILDDGNHPVDIVMTANQVLFKAE 192
_weihenstephanensis SHRLALRKAKIEGYNIADEFQANVVIPGKSLSELSK-ILDESEEMVDIVITEYQVLFRTK 239
*****:.*.** :*.. *****.**** **:.:. *****: *****:

EQ174 HLLFFSRLLDGNYPETARLIPTESKTTMIVNAKEFLQAIDRASLLAREGRNNVVKLTTLF 252
_weihenstephanensis HLLFFSRLLLEGNYPDTRLIPAESKTDIFVNTKEFLQAIDRASLLARDGRNNVVKLTSTLE 299
*****:***:****:***:***:***:*****:*****:*****:***

EQ174 GGMLEISSISPEIGKVTEQLQTESLEGEELNISFSAKYMMMDALRALDGTDIQISFTGAMR 312
_weihenstephanensis QOMLEISSNAPEIGKVVEEVQCENVDGEELKISFSAKYMMMDALKALDSTEIKVSFTGAMR 359
***** :*****.*::* *.:::****:*****.*****.*****

TQ174 PFLRLPFLHTDSMLQLILPVRTY 334
 _weihenstephanensis PFLIRTVNDDSIQLILPVRTY 381
 .*.: **

Sequence format is Pearson

Sequence 2: B subtilis 378 aa

Aligning...

```
Guide tree      file created:  [/ebi/extserv/clustalw-
```

Start of Multiple Alignment

Aligning...

Alignment Score 1379

```

SEQ174      -----NSDISIIIESFIPL 13
B_subtilis  MKFTIQKDRLVESVQDVLKAVSSRTTPIILTGIKIVASDDGVSETGSDSDIS-IESFIPK 59
                                     :**** *

```

```
SEQ174      ADEYPRLPQIEEENVFQIPADLLKTVIROTVFAVSTSETRPILTGWNWKVEHGELVCTAT   133  
B_subtilis ADEYPHPLQIEEHHAIQIPTDLLKNLIROTVFAVSTSETRPILTGWNWKEQSSELLCTAT   179  
*****.....*:***:*..:*****:~*****~*****~*****~*.**:****
```

```

SEQ174      LLFFSRLLDGNYPETARLIPTESKTTMIVNAKEFLQAI DRASLLAREGRNNVVKLTTLPG 253
B_subtilis VLFFSRLLDGNYPDTTSLIPQDSKTEIIVNTKEFLQAI DRASLLAREGRNNVVKLSAKPA 297
:*****: : * * * : * * * : * * * :*****: : *

```

```

SEQ174          FLLRPLHTDSMLQLILPVRTY 334
B_subtilis     FLIRTPNDETIVQLILPVRTY 378
                **:. : :. : *****

```

Sequence format is Pearson

```

SEQ174
B_licheniformis
-----NSDISIIIESFIPL 13
MKFTIQKDRLVESVDVLKAVSSRTTIPILTGIKIVASDEGVSLTGSDDIS-IESFIKP 59
:**** *****

SEQ174
B_licheniformis
EKEGKLLVDVKRPGSIVLQARFFSEIVKKLPQQTVEIETEDNFLTIIIRSGHSEFRLNGLN 73
EDGDLEIVTIEQPGSIVLQARFFSEIVKKLPMSTVEIEVQONQYLTIIIRSGKAEFNLNGLD 119
*. . :* ::*****.*****.:*:*****:*.****:

SEQ174
B_licheniformis
ADEYPRLPQIEEENVFQIPADLLKTVIRQTVFAVSTSETRPILTVGNWVKVEHGELVCTAT 133
ASEYPLLQPIEEHHAFQIPTDLLKNLIRQTVFAVSTSETRPILTVGNWNVTTGGELICTAT 179
*.*.*****.:****:****:*****:*****:*.***:****

SEQ174
B_licheniformis
DSHRLAMRKVKIIESENEVSNNVPIPGKSLNELSKIIILDDGNHPVDIVMTANQVLFKAEH 193
DSHRLALRKAKLDINE-DSSYNNVPIPGKSLTELSK-ILDDHQELVDIVITETQVLFKTKN 237
*****:*.*: .*: *****.***** ***** :. *****:*.*****::

SEQ174
B_licheniformis
LLFFSRLLDGNYPETARLIPTESKTTMIVNAKEFLQAI DRASLLAREGRNNVVKLTTLTPG 253
VLFFSRLLDGNYPDTNRLIPQESKTNLIVNTKEFLQAI DRASLLAREGRNNVVKLSAAAN 297
:*****:*.***** *****:***:*****:*****:*****:*. .

SEQ174
B_licheniformis
GMLEISSISPEIGKVTEQLQTESLEGEELNISFSAKYMMDALRALDGTDIQISTGAMRP 313
ESIEISSNSPEIGKVETVNAEQIEGEDLKISFSPKYM L DALKVLEGEDIHVSETGAMRP 357
:**** *****.* ::*:***:***:***:***:***:***:***:***:***:***:

SEQ174
B_licheniformis
FLLRPLHTDSMLQLILPVRTY 334
FLIRTPNDDSIQVILPVRTY 378
***. . :*:*****

```